

HCMI Searchable Catalog User Guide

What is the purpose of this document?

The purpose of this document is to provide users with a resource to effectively navigate the Human Cancer Models Initiative (HCMI) Searchable Catalog.

What is HCMI?

The Human Cancer Models Initiative (HCMI) is a collaboration between the US National Cancer Institute (NCI) – part of the National Institutes of Health (NIH), Cancer Research UK (CRUK), Wellcome Sanger Institute (WSI), and foundation Hubrecht Organoid Technology (HUB). The goal of HCMI is to create up to 1,000 next-generation cancer models from patient tumors that are clinically and molecularly characterized. For more information about the HCMI program, please visit: <https://ocg.cancer.gov/programs/HCMI>.

What is the HCMI Searchable Catalog?

The HCMI Searchable Catalog allows users to browse and identify potential next-generation cancer models generated by HCMI for use in research. Links to available associated molecular characterization data, clinical and biospecimen data at the National Cancer Institute's (NCI) Genomic Data Commons (GDC), the European Genome-phenome Archive (EGA), and the 3rd party HCMI Model Distributor are available on each model page as the information is processed and validated.

HCMI Searchable Catalog URL: <https://hcmi-searchable-catalog.nci.nih.gov/>

Supported browsers include Chrome, Firefox, and Edge.

Table of Contents

Navigating the HCMI Searchable Catalog Landing Page

What is displayed on the landing page?	2
How do I filter data elements to query the available models?	3
What do the graphs on the main viewing page indicate?	4
How can I download information regarding selected models?	5

Navigating Individual HCMI Model Pages

How can I save models from multiple searches for later use?	6
How do I navigate from one individual model page to the next?	7

Viewing Individual Model Data

How do I add models to "My Models List" from the individual model pages?	8
What information are available on individual model pages?	8
What information do additional categories include?	8
What information does the "VARIANTS" section contain?	9
Can the "VARIANTS" data be queried or downloaded?	9

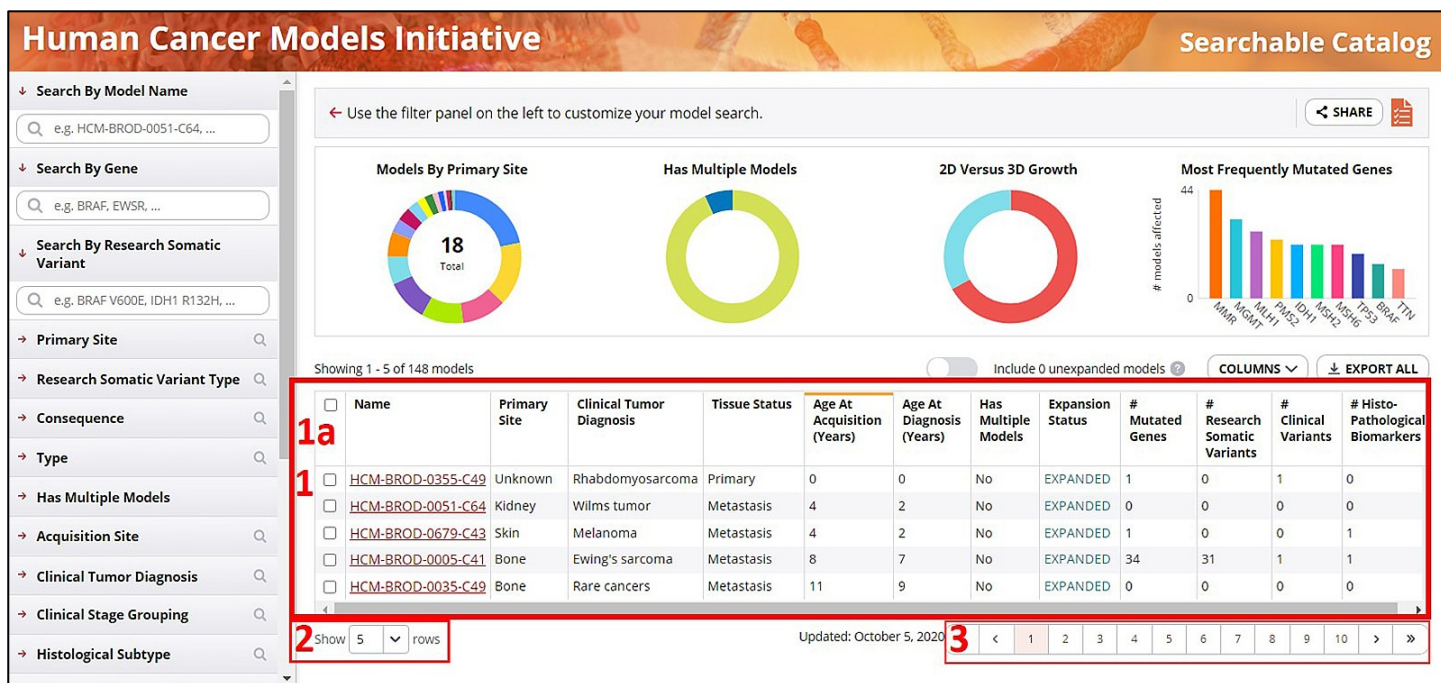
Feedback and Bug Reporting

Who do I contact if I have questions?	10
How do I report a bug?	10

Navigating the HCMI Searchable Catalog Landing Page

What is displayed on the landing page?

The landing page features a dynamic view, enabling users to filter the models by several elements, and easily download the saved results.



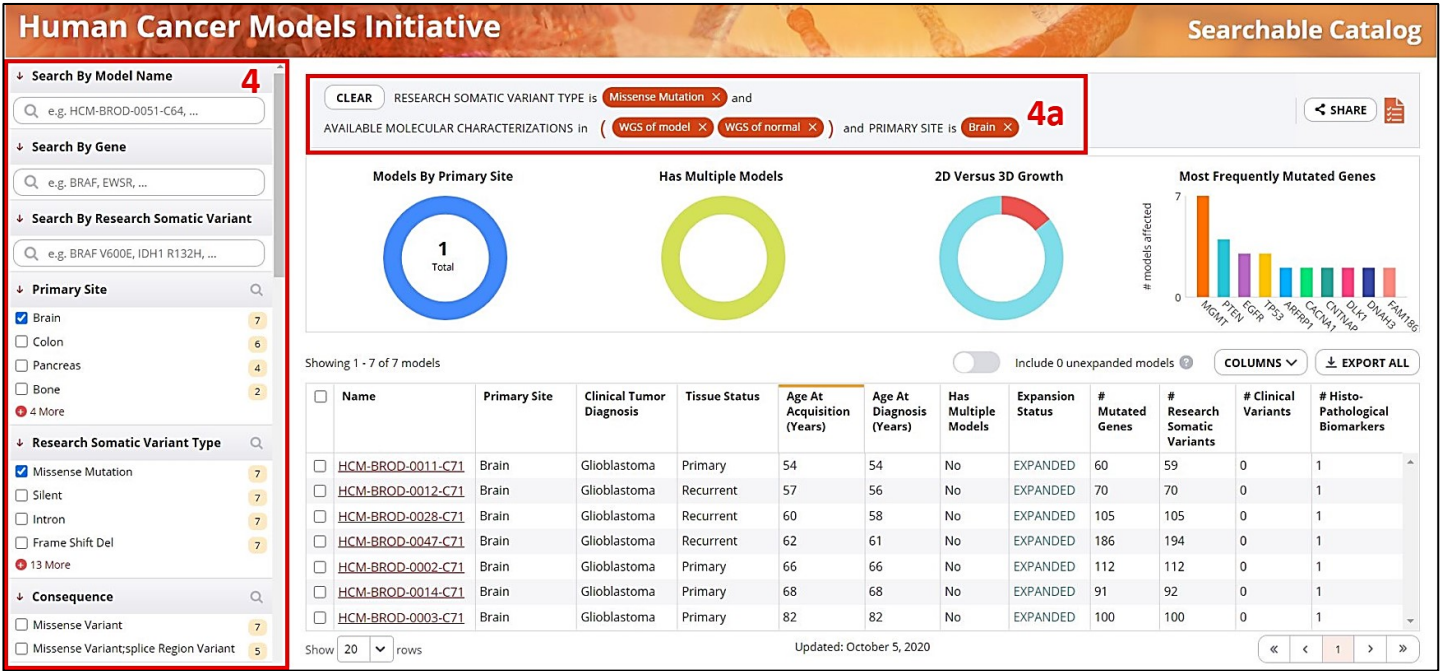
Box (1) shows the main viewing pane of the HCMI models. Users can sort the models in ascending or descending alphabetical or numerical order by clicking on the column headers such as “NAME”, “PRIMARY SITE”, etc.

Box (2) shows the number of models that users may choose to view.

Box (3) shows additional pages, if any, of available models.

Return to [Table of Contents](#)

Querying the Searchable Data Elements

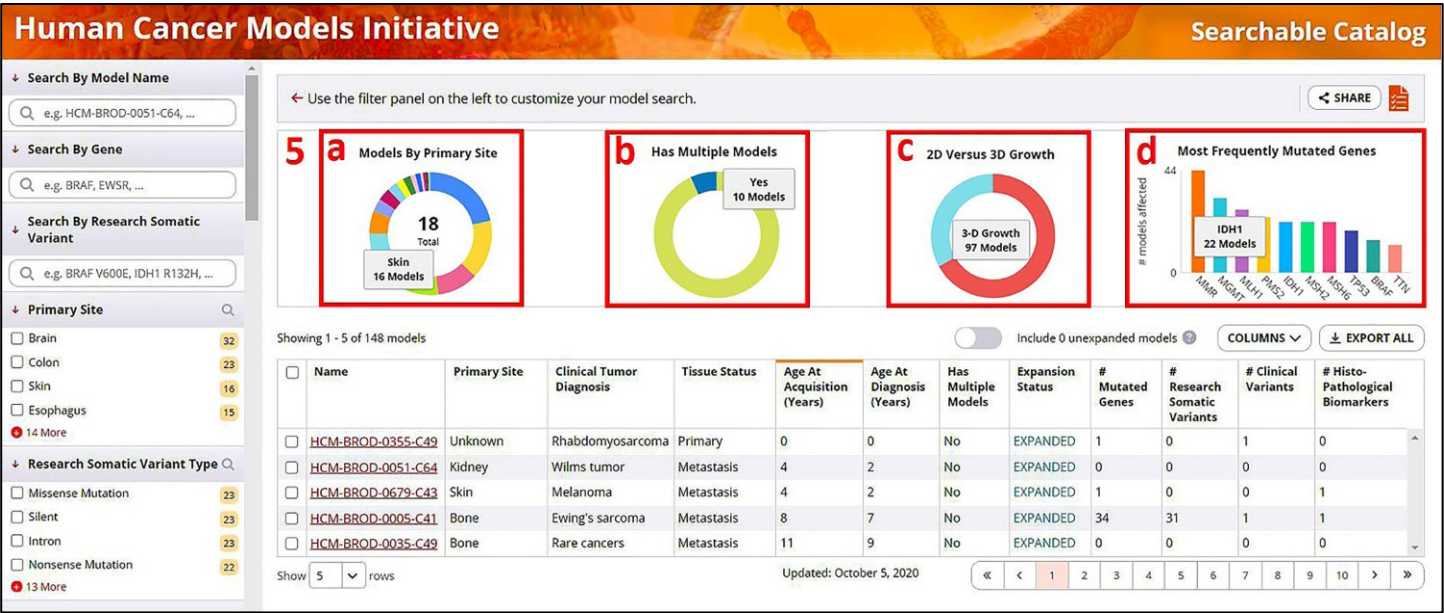


How do I filter data elements to query the available models?

Users may either search the models by typing in the model name, gene name or the research somatic variant type. Users may also filter the models using the data types displayed in Box (4) by checking or unchecking boxes to select or deselect data elements of interest. The list of models displayed in the main viewing pane and graphs will dynamically change as data elements in box (4) are selected or deselected.

Box (4a) at the top of the viewing pane shows the selected filtered data elements. Users may deselect a searchable data element by clicking the 'X' next to the name of the filtered element. To reset all selections, utilize the "CLEAR" button at the top of the pane.

Return to [Table of Contents](#)



What do the graphs on the main viewing page indicate?

Users may also filter the models by clicking on various colors within the interactive graphs shown in (5). Hovering over different colors within a graph will reveal relevant information.

Box (5a) shows that users can click on different colors within the circle graph and filter the models by primary sites of the available models. The example shown here highlights “Skin” as a primary site.

Box (5b) shows that users can select the models by whether the cases have multiple models derived from independent tumors from the same patient (e.g. primary and metastatic, primary and pre-malignant tissues, etc.) or not. The example shown here has the mouse hovered over the “blue” indicating the number of models that have multiple models.

Box (5c) shows that users can query the models by the growth type: 2-D or 3-D. The example shown here features 3-D models.

Box (5d) shows that users can query the models within the main viewing table by selecting the most frequently mutated gene(s). Users may select more than one gene at a time. The example shown here indicates the number of models with IDH1 mutation information.

Return to [Table of Contents](#)

Showing 1 - 5 of 148 models

<input type="checkbox"/>	Name	Primary Site	Clinical Tumor Diagnosis	Tissue Status	Age At Acquisition (Years)		
<input type="checkbox"/>	HCM-BROD-0355-C49	Unknown	Rhabdomyosarcoma	Primary	0	Primary Site	6
<input type="checkbox"/>	HCM-BROD-0051-C64	Kidney	Wilms tumor	Metastasis	4	Clinical Tumor Diagnosis	
<input type="checkbox"/>	HCM-BROD-0679-C43	Skin	Melanoma	Metastasis	4	Histological Subtype	
<input type="checkbox"/>	HCM-BROD-0005-C41	Bone	Ewing's sarcoma	Metastasis	8	Tissue Status	
<input type="checkbox"/>	HCM-BROD-0035-C49	Bone	Rare cancers	Metastasis	11	Acquisition Site	
						Gender	
						Race	
						Age At Acquisition (Years)	

COLUMNS ^

☒ Primary Site

☒ Clinical Tumor Diagnosis

☐ Histological Subtype

☒ Tissue Status

☐ Acquisition Site

☐ Gender

☐ Race

☒ Age At Acquisition (Years)

EXPORT ALL

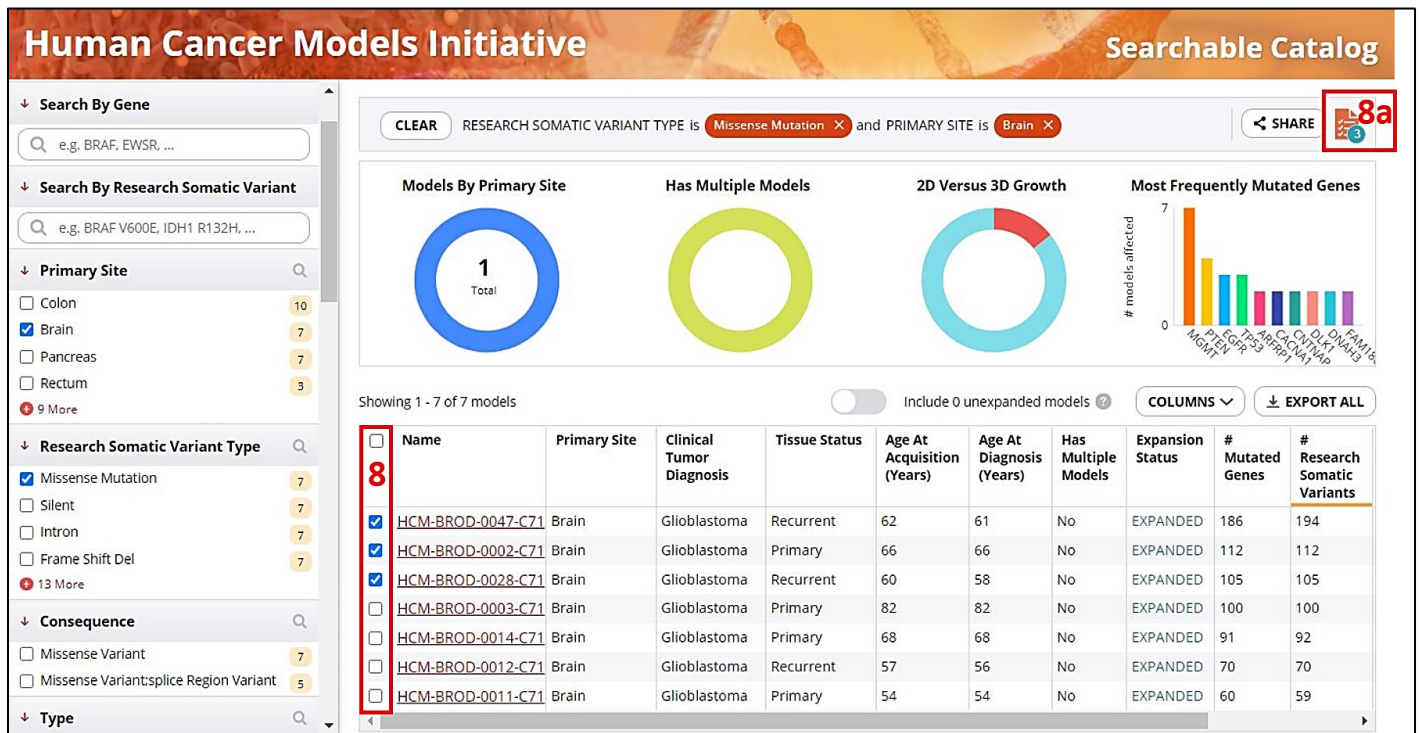
Mutated Genes
1
0
1
34
0

How can I download information regarding selected models?

The default columns shown in the main viewing pane can be customized based on information of interest. Users may select the data elements under the “**COLUMNS**” button shown in Box (6) to view in the main viewing pane.




Once users have selected the data elements to be shown in the viewing pane, these data can be exported using the “**EXPORT ALL**” function in box (7) and saved as a .tsv file. To view the .tsv file in a tabular format, users may open the saved file in Excel or similar program.




Return to [Table of Contents](#)



How can I save models from multiple searches for later use?

In box (8), users may select the models of interest by clicking on the checkboxes next to the model name. In the example shown, the “Primary Site” of “Brain” is selected. Users may further sort and select models that meet certain characteristics, for example, “# of Research Somatic Variants”. Selecting models adds them to the “My Model List” (box 8a), which functions as a ‘shopping list’. This feature may be helpful to users if multiple searches are conducted within a session. For example, if the user is also interested in models from the “Primary Site” of “Pancreas”, an additional search may be conducted, and further models may be added to “My Model List”.

<div> <div>»</div> <div>My Model List</div> <div>3</div> </div> <div> <div>CLEAR</div> </div>	
	<div>HCM-BROD-0011-C71</div> <div>Available:</div> <div>February 28, 2019</div> <div> <div></div> </div>
	<div>HCM-BROD-0012-C71</div> <div>Available:</div> <div>January 31, 2019</div> <div> <div></div> </div>
	<div>HCM-BROD-0028-C71</div> <div>Available:</div> <div>February 28, 2019</div> <div> <div></div> </div>

Clicking on the  icon in box (8a) allows users to view the models that have been saved to “My Model List”. Users may download the list of saved models by clicking the  **DOWNLOAD TSV** icon, individually delete the selected models by clicking the corresponding trash symbol,  , or clear all selected models from the list by clicking “**CLEAR**”.

Return to [Table of Contents](#)

Navigating Individual HCMI Model Pages

How do I navigate from one individual model page to the next?

To view an individual model page, users may select one of the models listed within the main viewing table by clicking on the model name of interest. In box (1), users may navigate to the previous or next individual model pages within the filtered list by clicking on the left/right arrows at the top or bottom of the page.

To return to the search results, users may select the “Back to Search” button located at the top of the page (box 2).

Human Cancer Models Initiative

Searchable Catalog

Model: **HCM-BROD-0011-C71**
EXPANDED

2
< BACK TO SEARCH
ADD MODEL TO MY LIST

1
< Previous
Model 1 of 1
Next >

MODEL DETAILS

Type
3-D: Other (e.g. neurosphere, air-liquid interface, etc.)
Split Ratio
1:2
Time to Split
N/A
Doubling Time
N/A
Tissue Status
Primary

MULTIPLE MODELS FROM THIS PATIENT (0)

There are no other models from this patient.

AVAILABLE MOLECULAR CHARACTERIZATIONS (8)

	Model	Tumor	Normal
WGS	✓	✓	✓
WXS	✓	✓	✓
Targeted-seq	✗	✗	✗
RNA-seq	✓	✓	✗

PATIENT DETAILS

Tissue Status	Primary
Gender	Male
Race	White
Age At Diagnosis (Years)	54
Age At Acquisition (Years)	54
Disease Status	Progressive disease
Vital Status	Dead
Neoadjuvant Therapy	No
Therapy	<ul style="list-style-type: none"> • Surgery • Cytotoxic chemotherapy • Targeted therapy (small molecule inhibitors and targeted antibodies) • Radiation therapy
Chemotherapeutic Drug List Available	Yes
Clinical Tumor Diagnosis	Glioblastoma
Histological Subtype	NOS
Primary Site	Brain
Acquisition Site	Brain
TNM Stage	N/A
Clinical Stage Grouping	N/A
Histological Grade	N/A

MODEL IMAGES (2)

Scale-bar length: 1000 µm | Magnification: 4 x

REPOSITORY STATUS

Date Updated	October 05, 2020
Date Of Availability	February 28, 2019
Licensing Required For Commercial Use	Yes
Date Created	December 03, 2018

EXTERNAL RESOURCES

SEQUENCING FILES
MODEL SOURCE

MASKED SOMATIC MAF

VISIT PDM-18 TO PURCHASE

VARIANTS

Research Somatic Variants
Showing 1 - 10 of 59 Variants
Filter
TSV

Variant	Gene	AA Change	Transcript	Consequence	Class	Type
chr1:g.2605576G>A	<u>MMEL1</u>	N266N	ENST00000378412	Synonymous Variant	SNV	SNP
chr1:g.117075643C>	<u>TFE2</u>	D353D	ENST00000369466	Synonymous Variant	SNV	SNP
chr1:g.176556357C>	<u>PAPPA2</u>	A12V	ENST00000367662	Missense Variant	SNV	SNP
chr1:g.237680495C>	<u>RYR2</u>	R2979C	ENST00000366574	Missense Variant	SNV	SNP
chr2:g.33727034A>C	<u>LINC01317</u>		ENST00000366209	Intron Variant;non C	SNV	SNP
chr2:g.200659197G>	<u>AOX1</u>	S1068S	ENST00000374700	Synonymous Variant	SNV	SNP
chr3:g.14466580C>T	<u>SLC6A6</u>	T266M	ENST00000622186	Missense Variant	SNV	SNP
chr3:g.38896972A>C	<u>SCN11A</u>	L759P	ENST00000302328	Missense Variant	SNV	SNP
chr3:g.129260771C>	<u>COPG1</u>	I364I	ENST00000314797	Synonymous Variant	SNV	SNP
chr3:g.197514250C>	<u>BDH1</u>		ENST00000358186	Intron Variant	SNV	SNP

1
< Previous
Model 1 of 1
Next >

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Sanger
HUB ORGANOID
CANCER RESEARCH UK

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Human Cancer Models Initiative

Searchable Catalog

Model: **HCM-BROD-0011-C71** EXPANDED
← BACK TO SEARCH
ADD MODEL TO MY LIST
3
3a

MODEL DETAILS

Type

3-D: Other (e.g. neurosphere, air-liquid interface, etc.)

Split Ratio

1:2

Time to Split

N/A

Doubling Time

N/A

Tissue Status

Primary

MULTIPLE MODELS FROM THIS PATIENT (0)

4

There are no other models from this patient.

AVAILABLE MOLECULAR CHARACTERIZATIONS (8)

	Model	Tumor	Normal
WGS	✓	✓	✓
WXS	✓	✓	✓
Targeted-seq	✗	✗	✗
RNA-seq	✓	✓	✗

PATIENT DETAILS

Tissue Status

Primary

Gender

Male

Race

White

Age At Diagnosis (Years)

54

Age At Acquisition (Years)

54

Disease Status

Progressive disease

Vital Status

Dead

Neoadjuvant Therapy

No

Therapy

- Surgery
- Cytotoxic chemotherapy
- Targeted therapy (small molecule inhibitors and targeted antibodies)
- Radiation therapy

Chemotherapeutic Drug List Available

Yes

Clinical Tumor Diagnosis

Glioblastoma

Histological Subtype

NOS

Primary Site

Brain

Acquisition Site

Brain

TNM Stage

N/A

Clinical Stage Grouping

N/A

Histological Grade

N/A

MODEL IMAGES (2)

Scale-bar length: 1000 µm | Magnification: 4 x

REPOSITORY STATUS

Date Updated

October 05, 2020

Date Of Availability

February 28, 2019

Licensing Required For Commercial Use

Yes

Date Created

December 03, 2018

EXTERNAL RESOURCES

5

SEQUENCING FILES

MODEL SOURCE

MASKED SOMATIC MAF

VISIT PDM-18 TO PURCHASE

How do I add models to “My Models List” from the individual model pages?

Individual models can be added to the “My Model List” by clicking ADD MODEL TO MY LIST (box 3). To view and download the saved models, click the “My Model List” icon (box 3a).

What information are available on individual model pages?

On each individual model page, all available data elements such as “MODEL DETAILS”, “PATIENT DETAILS”, and “MODEL IMAGES” are described.

What information do additional categories include?

“MULTIPLE MODELS FROM THIS PATIENT” (box 4) indicates whether there are other models derived from independent tumors from the same patient (e.g. primary and metastasis, primary and pre-malignant, primary and recurrent, etc.).

“EXTERNAL RESOURCES” (box 5) contains links to available sequencing data at the GDC, corresponding model page at the GDC, models’ masked somatic MAF data page, and the model distributor’s page.

VARIANTS

Showing 1 - 10 of 59 Variants

Research Somatic Variants (6)

Clinical Variants (7)

Histopathological Biomarkers (8)

Filter (9)

TSV (10)

Variant	Gene	AA Change	Transcript	Consequence	Class	Type
chr1:g.2605576G>A	MMEL1	N266N	ENST00000378412	Synonymous Variant	SNV	SNP
chr1:g.117075643C>	TTE2	D353D	ENST00000369466	Synonymous Variant	SNV	SNP
chr1:g.176556357C>	PAPPA2	A12V	ENST00000367662	Missense Variant	SNV	SNP
chr1:g.237680495C>	RYR2	R2979C	ENST00000366574	Missense Variant	SNV	SNP
chr2:g.33727034A>G	LINC01317		ENST00000366209	Intron Variant;non C	SNV	SNP
chr2:g.200659197G>	AOX1	S1068S	ENST00000374700	Synonymous Variant	SNV	SNP
chr3:g.14466580C>T	SLC6A6	T266M	ENST00000622186	Missense Variant	SNV	SNP
chr3:g.38896972A>G	SCN11A	L759P	ENST00000302328	Missense Variant	SNV	SNP
chr3:g.129260771C>	COPG1	I364I	ENST00000314797	Synonymous Variant	SNV	SNP
chr3:g.197514250C>	BDH1		ENST00000358186	Intron Variant	SNV	SNP

Show 10 rows

Previous Model 1 of 1 Next

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What information does the “VARIANTS” section contain?

The “VARIANTS” section contains available “Research Somatic Variants”, “Clinical Variants”, and “Histopathological Biomarkers” data tabs. The data columns within each tab can be sorted either in ascending or descending order by clicking on the column header of interest.

“Research Somatic Variants” tab (box 6) shows available open-access masked somatic MAF variant data at the GDC. As part of GDC’s harmonization process, potential germline mutations are filtered from the variants identified by DNA sequencing of the model and normal tissues. These highly-filtered lists of somatic mutations without the germline variants are called “masked somatic mutations”. The masked somatic mutations generated at GDC for each model are shown as “Research Somatic Variants” on the Catalog. Catalog users may search the available models for gene mutations of interest. If omission of true-positive somatic mutations is a concern, it is recommended that users access the controlled-access MAF files housed at the GDC. Access to controlled-access data is granted through dbGaP. Visit the [Accessing HCMC Data](#) page for more information.

The “Clinical Variants” tab (box 7) shows available clinical variants reported from clinical sequencing of the tumor collected from the clinical record.

The “Histopathological Biomarkers” tab (box 8) shows the results of reported clinical histopathological biomarkers collected from the clinical record.

Can the “VARIANTS” data be queried or downloaded?

In box (9), users may filter the “VARIANTS” information on each tab by entering querying text (e.g. MSH6, TP53, etc.). Users may download the variant information by clicking the icon (box 10).

Return to [Table of Contents](#)

Additional Help, Feedback, and Bug Reporting



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Who do I contact if I have questions?

For questions, users may visit the HCMI FAQs page by clicking the “**Help**” button at the bottom of the webpage.

How do I report a bug?

Users may provide feedback or report bugs directly to the Office of Cancer Genomics by emailing: ocg@mail.nih.gov or by clicking “**Contact Us**” at the bottom of the Catalog webpage.

Return to [Table of Contents](#)